RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/774,378
Source: IFW16
Date Processed by STIC: 10/24/07

ENTERED

IFW16

RAW SEQUENCE LISTING DATE: 10/24/2007
PATENT APPLICATION: **US/10/774,378** TIME: 11:56:15

Input Set : **A:\10774378.txt**
Output Set: **N:\CRF4\10242007\J774378.raw**

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      2 <110> APPLICANT: Ono Pharmaceutical Co., Ltd.
      4 <120> TITLE OF INVENTION: Novel Polypeptides, DNAs encoding the polypeptides, and
utility of the
      5       Polypeptides
      7 <130> FILE REFERENCE: Q55589
      9 <140> CURRENT APPLICATION NUMBER: 10/774,378
     10 <141> CURRENT FILING DATE: 2004-02-10
     12 <150> PRIOR APPLICATION NUMBER: 09/380,276
     13 <151> PRIOR FILING DATE: 1999-08-27
     15 <150> PRIOR APPLICATION NUMBER: JP 9-43143
     16 <151> PRIOR FILING DATE: 1997-02-27
     18 <150> PRIOR APPLICATION NUMBER: PCT/JP98/00799
     19 <151> PRIOR FILING DATE: 1997-02-27
     21 <160> NUMBER OF SEQ ID NOS: 10
     23 <170> SOFTWARE: PatentIn version 3.0
     25 <210> SEQ ID NO: 1
     26 <211> LENGTH: 1251
     27 <212> TYPE: DNA
     28 <213> ORGANISM: Homo Sapiens
     30 <400> SEQUENCE: 1
     31 atggctttaa aagtgctact agaacaagag aaaacgtttt tcactctttt agtattacta     60
     33 ggctatttgt catgtaaagt gacttgtgaa acaggagact gtagacagca agaattcagg    120
     35 gatcggtctg gaaactgtgt tccctgcaac cagtgtgggc caggcatgga gttgtctaag    180
     37 gaatgtggct tcggctatgg ggaggatgca cagtgtgtga cgtgccggct gcacaggttc    240
     39 aaggaggact ggggcttcca gaaatgcaag ccctgtctgg actgcgcagt ggtgaaccgc    300
     41 tttcagaagg caaattgttc agccaccagt gatgccatct gcggggactg cttgccagga    360
     43 ttttatagga agacgaaact tgtcggcttt caagacatgg agtgtgtgcc ttgtggagac    420
     45 cctcctcctc cttacgaacc gcactgtgcc agcaaggtca acctcgtgaa gatcgcgtcc    480
     47 acggcctcca gcccacggga cacggcgctg gctgccgtta tctgcagcgc tctggccacc    540
     49 gtcctgctgg ccctgctcat cctctgtgtc atctattgta agagacagtt tatggagaag    600
     51 aaacccagct ggtctctgcg gtcacaggac attcagtaca acggctctga gctgtcgtgt    660
     53 cttgacagac ctcagctcca cgaatatgcc cacagagcct gctgccagtg ccgccgtgac    720
     55 tcagtgcaga cctgcgggcc ggtgcgcttg ctcccatcca tgtgctgtga ggaggcctgc    780
     57 agccccaacc cggcgactct tggttgtggg gtgcattctg cagccagtct tcaggcaaga    840
     59 aacgcaggcc cagccgggga gatggtgccg actttcttcg gatccctcac gcagtccatc    900
     61 tgtggcgagt tttcagatgc ctggcctctg atgcagaatc ccatgggtgg tgacaacatc    960
     63 tctttttgtg actcttatcc tgaactcact ggagaagaca ttcattctct caatccagaa   1020
     65 cttgaaagct caacgtcttt ggattcaaat agcagtcaag atttggttgg tggggctgtt   1080
     67 ccagtccagt ctcattctga aaactttaca gcagctactg atttatctag atataacaac   1140
     69 acactggtag aatcagcatc aactcaggat gcactaacta tgagaagcca gctagatcag   1200
     71 gagagtggcg ctatcatcca cccagccact cagacgtccc tccaggaagc t            1251
     73 <210> SEQ ID NO: 2
     74 <211> LENGTH: 1704
     75 <212> TYPE: DNA
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76 <213> ORGANISM: Homo sapiens
78 <400> SEQUENCE: 2
79 gggaacgtag aactctccaa caataaatac atttgataag aaagatggct ttaaaagtgc 60
81 tactagaaca agagaaaacg tttttcactc ttttagtatt actaggctat ttgtcatgta 120
83 aagtgacttg tgaaacagga gactgtagac agcaagaatt cagggatcgg tctggaaact 180
85 gtgttccctg caaccagtgt gggccaggca tggagttgtc taaggaatgt ggcttcggct 240
87 atggggagga tgcacagtgt gtgacgtgcc ggctgcacag gttcaaggag gactggggct 300
89 tccagaaatg caagccctgt ctggactgcg cagtggtgaa ccgctttcag aaggcaaatt 360
91 gttcagccac cagtgatgcc atctgcgggg actgcttgcc aggattttat aggaagacga 420
93 aacttgtcgg ctttcaagac atggagtgtg tgccttgtgg agaccctcct cctccttacg 480
95 aaccgcactg tgccagcaag gtcaacctcg tgaagatcgc gtccacggcc tccagcccac 540
97 gggacacggc gctggctgcc gttatctgca gcgctctggc caccgtcctg ctggccctgc 600
99 tcatcctctg tgtcatctat tgtaagagac agtttatgga gaagaaaccc agctggtctc 660
101 tgcggtcaca ggacattcag tacaacggct ctgagctgtc gtgtcttgac agacctcagc 720
103 tccacgaata tgcccacaga gcctgctgcc agtgccgccg tgactcagtg cagacctgcg 780
105 ggccggtgcg cttgctccca tccatgtgct gtgaggaggc ctgcagcccc aacccggcga 840
107 ctcttggttg tggggtgcat tctgcagcca gtcttcaggc aagaaacgca ggcccagccg 900
109 gggagatggt gccgactttc ttcggatccc tcacgcagtc catctgtggc gagttttcag 960
111 atgcctggcc tctgatgcag aatcccatgg gtggtgacaa catctctttt tgtgactctt 1020
113 atcctgaact cactggagaa gacattcatt ctctcaatcc agaacttgaa agctcaacgt 1080
115 ctttggattc aaatagcagt caagatttgg ttggtggggc tgttccagtc cagtctcatt 1140
117 ctgaaaactt tacagcagct actgatttat ctagatataa caacacactg gtagaatcag 1200
119 catcaactca ggatgcacta actatgagaa gccagctaga tcaggagagt ggcgctatca 1260
121 tccacccagc cactcagacg tccctccagg aagcttaaag aacctgcttc tttctgcagt 1320
123 agaagcgtgt gctggaaccc aaagagtact cctttgttag gcttatggac tgagcagtct 1380
125 ggaccttgca tggcttctgg ggcaaaaata aatctgaacc aaactgacgg catttgaagc 1440
127 ctttcagcca gttgcttctg agccagacca gctgtaagct gaaacctcaa tgaataacaa 1500
129 gaaaagactc caggccgact catgatactc tgcatctttc ctacatgaga agcttctctg 1560
131 ccacaaaagt gacttcaaag acggatgggt tgagctggca gcctatgaga ttgtggacat 1620
133 ataacaagaa acagaaatgc cctcatgctt attttcatgg tgattgtggt tttacaagac 1680
135 tgaagaccca gagtatactt tttc 1704
138 <210> SEQ ID NO: 3
139 <211> LENGTH: 1704
140 <212> TYPE: DNA
141 <213> ORGANISM: Homo sapiens
143 <220> FEATURE:
144 <221> NAME/KEY: misc_feature
145 <223> OTHER INFORMATION: Origin: human bone marrow stromal cell line HAS303
148 <220> FEATURE:
149 <221> NAME/KEY: CDS
150 <222> LOCATION: (45)..(1295)
152 <220> FEATURE:
153 <221> NAME/KEY: sig_peptide
154 <222> LOCATION: (45)..(119)
156 <220> FEATURE:
157 <221> NAME/KEY: mat_peptide
158 <222> LOCATION: (120)..(1295)
160 <400> SEQUENCE: 3
161 gggaacgtag aactctccaa caataaatac atttgataag aaag atg gct tta aaa 56

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Input Set : **A:\10774378.txt**
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```
                                                    Met Ala Leu Lys
                                                    -25
gtg cta cta gaa caa gag aaa acg ttt ttc act ctt tta gta tta cta      104
Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu Leu Val Leu Leu
    -20                 -15                 -10
ggc tat ttg tca tgt aaa gtg act tgt gaa aca gga gac tgt aga cag      152
Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly Asp Cys Arg Gln
-5              -1  1               5                   10
caa gaa ttc agg gat cgg tct gga aac tgt gtt ccc tgc aac cag tgt      200
Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro Cys Asn Gln Cys
            15                  20                  25
ggg cca ggc atg gag ttg tct aag gaa tgt ggc ttc ggc tat ggg gag      248
Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly Glu
        30                  35                  40
gat gca cag tgt gtg acg tgc cgg ctg cac agg ttc aag gag gac tgg      296
Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe Lys Glu Asp Trp
    45                  50                  55
ggc ttc cag aaa tgc aag ccc tgt ctg gac tgc gca gtg gtg aac cgc      344
Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala Val Val Asn Arg
60                  65                  70                  75
ttt cag aag gca aat tgt tca gcc acc agt gat gcc atc tgc ggg gac      392
Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala Ile Cys Gly Asp
                80                  85                  90
tgc ttg cca gga ttt tat agg aag acg aaa ctt gtc ggc ttt caa gac      440
Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln Asp
            95                  100                 105
atg gag tgt gtg cct tgt gga gac cct cct cct cct tac gaa ccg cac      488
Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro Tyr Glu Pro His
        110                 115                 120
tgt gcc agc aag gtc aac ctc gtg aag atc gcg tcc acg gcc tcc agc      536
Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser Thr Ala Ser Ser
    125                 130                 135
cca cgg gac acg gcg ctg gct gcc gtt atc tgc agc gct ctg gcc acc      584
Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser Ala Leu Ala Thr
140                 145                 150                 155
gtc ctg ctg gcc ctg ctc atc ctc tgt gtc atc tat tgt aag aga cag      632
Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr Cys Lys Arg Gln
                160                 165                 170
ttt atg gag aag aaa ccc agc tgg tct ctg cgg tca cag gac att cag      680
Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser Gln Asp Ile Gln
            175                 180                 185
tac aac ggc tct gag ctg tcg tgt ctt gac aga cct cag ctc cac gaa      728
Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro Gln Leu His Glu
        190                 195                 200
tat gcc cac aga gcc tgc tgc cag tgc cgc cgt gac tca gtg cag acc      776
Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp Ser Val Gln Thr
    205                 210                 215
tgc ggg ccg gtg cgc ttg ctc cca tcc atg tgc tgt gag gag gcc tgc      824
Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys Glu Glu Ala Cys
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227 220                 225                 230                 235
229 agc ccc aac ccg gcg act ctt ggt tgt ggg gtg cat tct gca gcc agt      872
230 Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His Ser Ala Ala Ser
231                 240                 245                 250
233 ctt cag gca aga aac gca ggc cca gcc ggg gag atg gtg ccg act ttc      920
234 Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met Val Pro Thr Phe
235             255                 260                 265
237 ttc gga tcc ctc acg cag tcc atc tgt ggc gag ttt tca gat gcc tgg      968
238 Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe Ser Asp Ala Trp
239         270                 275                 280
241 cct ctg atg cag aat ccc atg ggt ggt gac aac atc tct ttt tgt gac     1016
242 Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile Ser Phe Cys Asp
243     285                 290                 295
245 tct tat cct gaa ctc act gga gaa gac att cat tct ctc aat cca gaa     1064
246 Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser Leu Asn Pro Glu
247 300                 305                 310                 315
249 ctt gaa agc tca acg tct ttg gat tca aat agc agt caa gat ttg gtt     1112
250 Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser Gln Asp Leu Val
251                 320                 325                 330
253 ggt ggg gct gtt cca gtc cag tct cat tct gaa aac ttt aca gca gct     1160
254 Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn Phe Thr Ala Ala
255             335                 340                 345
257 act gat tta tct aga tat aac aac aca ctg gta gaa tca gca tca act     1208
258 Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu Ser Ala Ser Thr
259         350                 355                 360
261 cag gat gca cta act atg aga agc cag cta gat cag gag agt ggc gct     1256
262 Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln Glu Ser Gly Ala
263     365                 370                 375
265 atc atc cac cca gcc act cag acg tcc ctc cag gaa gct taaagaacct      1305
266 Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu Ala
267 380                 385                 390
269 gcttctttct gcagtagaag cgtgtgctgg aacccaaaga gtactccttt gttaggctta   1365
271 tggactgagc agtctggacc ttgcatggct tctggggcaa aaataaatct gaaccaaact   1425
273 gacggcattt gaagcctttc agccagttgc ttctgagcca gaccagctgt aagctgaaac   1485
275 ctcaatgaat aacaagaaaa gactccaggc cgactcatga tactctgcat ctttcctaca   1545
277 tgagaagctt ctctgccaca aaagtgactt caaagacgga tgggttgagc tggcagccta   1605
279 tgagattgtg gacatataac aagaaacaga aatgccctca tgcttatttt catggtgatt   1665
281 gtggttttac aagactgaag acccagagta tacttttc                          1704
284 <210> SEQ ID NO: 4
285 <211> LENGTH: 417
286 <212> TYPE: PRT
287 <213> ORGANISM: Homo sapiens
289 <220> FEATURE:
290 <221> NAME/KEY: misc_feature
291 <223> OTHER INFORMATION: Origin: human bone marrow stromal cell line HAS303
293 <400> SEQUENCE: 4
295 Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu
296 -25                 -20                 -15                 -10
299 Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly
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```
300                 -5              -1  1               5
303 Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
304         10                  15                  20
307 Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
308     25                  30                  35
311 Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
312 40                  45                  50                  55
315 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala
316                 60                  65                  70
319 Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala
320             75                  80                  85
323 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
324         90                  95                  100
327 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
328     105                 110                 115
331 Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser
332 120                 125                 130                 135
335 Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
336                 140                 145                 150
339 Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
340             155                 160                 165
343 Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser
344         170                 175                 180
347 Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro
348     185                 190                 195
351 Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp
352 200                 205                 210                 215
355 Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys
356                 220                 225                 230
359 Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His
360             235                 240                 245
363 Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met
364         250                 255                 260
367 Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe
368     265                 270                 275
371 Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile
372 280                 285                 290                 295
375 Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser
376                 300                 305                 310
379 Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser
380             315                 320                 325
383 Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn
384         330                 335                 340
387 Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu
388     345                 350                 355
391 Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln
392 360                 365                 370                 375
395 Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu
396                 380                 385                 390
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/24/2007
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 27,28,29,30,31,32,33,34,35

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:9,10

VERIFICATION SUMMARY DATE: 10/24/2007
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L:786 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9
L:786 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0